

FIG. 1A

ctcgtcctctcctacttggataactgtggtaattctagagctaatacatgccgacgggc 60
gctgaccccccttcgcgggggggatgctgcatthtatcagatcaagaccaaccgggtcagc 120
ccctctccggcccccgccggggggcgggcgccggcggtttggtgactctagataacctc 180
gggccgatcgacgccccccgtggcgggcgacgaccattcgaacgtctgccctatcaact 240
ttcgatggtagtcgccgtgcctaccatggtgaccacgggtgacggggaatcagggttcga 300
ttccggagagggagcctgagaaacggctaccacatccaaggaaggcagcaggcgcgcaaa 360
ttaccactcccggaggtggcgggcgcccatcttggcgaaggggggatcaggaagtgcg 420
gaccgcggcgggcgggcgggcgggcgggcgggcgagcccgagcgcaggccggaggctc 480
ccggcccgcggcccccgagcggagcggagcggaggatgcagcagccgcagccgcagggg 540
cagcagcagccggggccggggcagcagctggggggccagggggcggcggggggccggg 600
ggcgggccagggggggggcccgggggccggggccctgcctgaggcgagagctgaagctgctc 660
gagtcctatctccaccgcggccacgagcgttccgcattgccagcgctgcctggacgag 720
ctgagctgcgagttcctgctggctggggccggagggggccggggcgggggccgcgccgga 780
ccgcctctccccccacgggggtcggtgcctggggatcctgtccgcctccactgcaacatc 840
acggagtcataccctgctgtgccccccatctggtcggtggagctctgatgaccctaacttg 900
gctgctgtcttgagaggctggtggacataaagaaaggaataactctgctattgcagcat 960
ctgaagaggatcatctccgacctgtgtaaaactctataacctccctcagcatccagatgtg 1020
gagatgctggatcaacccttgccagcagagcagtgccacaggaagacgtgtcttcagaa 1080
gatgaagatgaggagatgcctgaggacacagaagacttagatcactatgaaatgaaagag 1140
gaagagccagctgagggcaagaaatctgaagatgatggcattggaaaagaaaacttggcc 1200
atcctagagaaaattaaaaagaaccagaggcaagattacttaaagtgtgcagtgtctggc 1260
tcggtgcaggccactgaccggctgatgaaggagctcagggatataaccgatcacagagt 1320
ttcaaaggcggaactatgcagtcgaactcgtgaatgacagctctgtatgattggaatgtc 1380
aaactcctcaaagttgaccaggacagcgctttgcacaacgatctccagatcctcaaagag 1440

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FIG. 1B

aaagaaggagccgacttcattctacttaacttttcctttaagataactttccctttgac 1500
ccaccatttgtcaggggtgtgtctccagtcctctctggagggatgttctgggcggaggg 1560
gccatctgcatggaacttctcaccaaacagggctggagcagtgccctactccatagagtca 1620
gtgatcatgcagatcagtgccacactgggtgaaggggaaagcacgagtgagttggagcc 1680
aacaaatctcaatacagtctgacaagagcacagcagtcctacaagtccttggtgcagatc 1740
cacgaaaaaaaaacggctggtacacaccccccaaaagaagacggctaaccctggagtatcacc 1800
cttcctccctccccaggcaccactggaccaattacctttgaatgctgtatttggaatctca 1860
cgctgcctctgtggttcctccctcatttttctggacgtgatagctctgcctattgcag 1920
gacaatgatggctattctaaacgctaaggaaaaaaaaacaaacacagaactgtttcaagta 1980
ctcaagactgacttacagaccaaccaaccaccttgctggaacccttgctagcaggcattc 2040
ttataaaagaaactttcgagcctccttatattgctggaaactcagctgtgctccagacta 2100
gagcctccttacctatgctatggatttttaattttattttctcttatttcattgtactgc 2160
tttttttggttacagtgtatgatggatgtgtatgaaaaaatgtatctttgggaaaacaa 2220
ttacagtttggttaatttgaaaaaaaaaaaaaaaaa 2280

(SEQ ID NO:1)

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FIG. 2A

CTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATACATGCCGACGGGC
GCTGACCCCTTCGCGGGGGGGATGCGTGCATTTATCAGATCAAGACCAACCCGGTCAGC
CCCTCTCCGGCCCCCGCGGGGGGGCGGGCGCCGGCGGCTTTGGTGA CTCTAGATAACCTC
GGGCCGATCGCACGCCCCCGTGGCGGCGACGACCATTCGAACGTCTGCCCTATCAACT
TTCGATGGTAGTCGCCGTGCCTACCATGGTGACCACGGGTGACGGGGAATCAGGGTTCTGA
TTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAA
TTACCCACTCCCGGAGGTGGCGGCGGCGCCATCTTGGCGAAGGGGGGATCAGGAAGTGCG
GACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGCCCGAGCGCAGGCGCGGAGGCTC
CCGGCCCCGCGGCCCCCGGAGCGGAGCGGAGCGGAGGATGCAGCAGCCGAGCCGAGGGG
M Q Q P Q P Q G
CAGCAGCAGCCGGGGCCGGGGCAGCAGCTGGGGGGCCAGGGGGCGGCGCCGGGGCCGGG
Q Q Q P G P G Q Q L G G Q G A A P G A G
GGCGGCCAGGGGGGGCCCCGGGGCCGGGGCCCTGCCTGAGGCGAGAGCTGAAGCTGCTC
G G P G G G P G P G P C L R R E L K L L
GAGTCCATCTTCCACCGCGGCCACGAGCGCTTCCGCATTGCCAGCGCCTGCCTGGACGAG
E S I F H R G H E R F R I A S A C L D E
CTGAGCTGCGAGTTCTGCTGGCTGGGGCCGAGGGGGCCGGGGCGGGGGCCGCGCCCCGA
L S C E F L L A G A G G A G A G A A P G
CCGCATCTCCCCCACGGGGGTGCGTGCCTGGGGATCCTGTCCGCATCCACTGCAACATC
P H L P P R G S V P G D P V R I H C N I
ACGGAGTCATACCCTGCTGTGCCCCCATCTGGTGGTGGAGTCTGATGACCCTAACTTG
T E S Y P A V P P I W S V E S D D P N L
GCTGCTGTCTTGGAGAGGCTGGTGGACATAAAGAAAGGAATACTCTGCTATTGCAGCAT
A A V L E R L V D I K K G N T L L L Q H
CTGAAGAGGATCATCTCCGACCTGTGTAAACTCTATAACCTCCCTCAGCATCCAGATGTG
L K R I I S D L C K L Y N L P Q H P D V
GAGATGCTGGATCAACCTTGCCAGCAGAGCAGTGCACACAGGAAGACGTGTCTTCAGAA
E M L D Q P L P A E Q C T Q E D V S S E
GATGAAGATGAGGAGATGCCTGAGGACACAGAAGACTTAGATCACTATGAAATGAAAGAG
D E D E E M P E D T E D L D H Y E M K E
GAAGAGCCAGCTGAGGGCAAGAAATCTGAAGATGATGGCATTGGAAAAGAAAATCTGGCC
E E P A E G K K S E D D G I G K E N L A
ATCCTAGAGAAAATTAAAAAGAACCAGAGGCAAGATTACTTAAATGGTGCAGTGTCTGGC
I L E K I K K N Q R Q D Y L N G A V S G
TCGGTGCAGGCCACTGACCGGTGATGAAGGAGCTCAGGGATATATACCGATCACAGAGT
S V Q A T D R L M K E L R D I Y R S Q S
TTCAAAGGCGGAAACTATGCAGTCGAACTCGTGAATGACAGTCTGTATGATTGGAATGTC
F K G G N Y A V E L V N D S L Y D W N V
AAACTCCTCAAAGTTGACCAGGACAGCGCTTTGCACAACGATCTCCAGATCCTCAAAGAG
K L L K V D Q D S A L H N D L Q I L K E
AAAGAAGGAGCCGACTTCATTCTACTTAACTTTTCCTTTAAAGATAACTTTCCCTTTGAC
K E G A D F I L L N F S F K D N F P F D
CCACCATTTGTCAGGGTTGTGTCTCCAGTCCTCTCTGGAGGGTATGTTCTGGGCGGAGGG
P P F V R V V S P V L S G G Y V L G G G
GCCATCTGCATGGAACCTCTCACCAAACAGGGCTGGAGCAGTGCCTACTCCATAGAGTCA
A I C M E L L T K Q G W S S A Y S I E S
GTGATCATGCAGATCAGTGCCACACTGGTGAAGGGGAAAGCACGAGTGCAGTTTGGAGCC
V I M Q I S A T L V K G K A R V Q F G A

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FIG. 2B

AACAAATCTCAATACAGTCTGACAAGAGCACAGCAGTCCTACAAGTCCTTGGTGCAGATC
N K S Q Y S L T R A Q Q S Y K S L V Q I
CACGAAAAAACGGCTGGTACACACCCCCAAAAGAAGACGGCTAACCCCTGGAGTATCACC
H E K N G W Y T P P K E D G *
CTTCCTCCCTCCCCAGGCACCACTGGACCAATTACCTTTGAATGCTGTATTTGGATCTCA
CGCTGCCTCTGTGGTTCCCTCCCTCATTTTTCCTGGACGTGATAGCTCTGCCTATTGCAG
GACAATGATGGCTATTCTAAACGCTAAGGAAAAAAAACAAACACAGAACTGTTTCAAGTA
CTCAAGACTGACTTACAGACCAACCAACCACCTTGCTGGAACCCCTTGCTAGCAGGCATTC
TTATAAAAGAAACTTTTCGAGCCTCCTTATATTGCTGGAACTCAGCTGTGCTCCAGACTA
GAGCCTCCTTACCTATGCTATGGATTTTAAATTTATTTTCTCTTATTTTCATGTACACTGC
TTTTTTTGGTTACAGTGTATGATGGATGTGTATGAAAAAATGTATCTTTGGGAAAACAA
TTACAGTTTGTTAATTTGAAAAAAAAAAAAAAAAA

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FIG. 3

MQQPQPQGQQ	QPGPGQQLGG	QGAAPGAGGG	PGGGPGPGPC	40
LRRELKLLS	IFHRGHERFR	IASACLDELS	CEFLAGAGG	80
AGAGAAPGPH	LPPRGSVPGD	PVRIHCNITE	SYPAVPPIWS	120
VESDDPNLAA	VLERLVDIKK	GNTLLLQHLK	RIISDLCKLY	160
NLPQHDPDEM	LDQPLPAEQC	TQEDVSSSEDE	DEEMPEDTED	200
LDHYEMKEEE	PAEGKKSEDD	GIGKENLAIL	EKIKKNQRQD	240
YLNGAVSGSV	QATDRLMKEL	RDIYRSQSFK	GGNYAVELVN	280
DSLVDWNVKL	LKVDQDSALH	NDLQILKEKE	GADFILLNFS	320
FKDNFPFDPP	FVRVVSPLS	GGYVLGGGAI	CMELLTKQGW	360
SSAYSIESVI	MQISATLVKG	KARVQFGANK	SQYSLTRAQQ	400
SYKSLVQIHE	KNGWYTPPKE	DG		422

(SEQ ID NO:2)

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FIG. 4

1 65

RATL1d6 (1) MQQPQPQGGQPGPGQQLGGQGAAPGAGGGPGGGPGPGPCLRRELKLLSIFHRGHIERFRIASAC

T21349_F25H2.8_Cel (1) -----MACLRKLKEDIQVLEKLFPKNHNRFQILSAS

AAF45767_EG:25E8_Dr (1) -----MACLNTLKQEIKTLEKIFPKNHERFQILNSS

66 130

RATL1d6 (66) LDELSCEBLLAGAGGAGAGAAPGPHLPPRGSVPGDPVRIHCHITISYPAPVPIWSVESDDPNLAA

T21349_F25H2.8_Cel (32) VDELSMKFINAEN-----KG-----IIVTANIQENYPRQPPPIWFSESDDVPVIG

AAF45767_EG:25E8_Dr (32) VDELLCRFIDKNG-----KR-----YDIHANITETYEISSPPVWFAESEETSVTN

131 195

RATL1d6 (131) VLERLVDIKKNTLLQLHLKRIISDLCKLYNLPHQHPDVEMLDQPL-----

T21349_F25H2.8_Cel (76) MSLQRLTETEESTNLIHQVHRLVSDLCFSYNLQMPCELPQIAPFVRDD-----IDEGRGSDI

AAF45767_EG:25E8_Dr (76) AVQILSNTNGRDNHVINQVGILLRELCLRLHNVLPPDIDNLALPLQTPPPSASPLRCEQRPGGGG

196 260

RATL1d6 (176) -----PAEQCTQEDVSSSEDEDEEMPEDTEDLDHYEMKEEPAEGKKSSEDDGIGKENLAILEKIK

T21349_F25H2.8_Cel (133) SDTTSEPIDDDMAGDGEVDDDDDEEEDDEDADGDIEIVEMAEDPTSQHDVGVSKEGLDMLDKVS

AAF45767_EG:25E8_Dr (141) AGGGGGPHGNEETSDSQEEIEDPIGESEGESEGEDDLPLEMDDDRSTSKDDMEVEHLATLEKLR

P52483_UB6B_MOUSE (1) -----MSSDRQRSDDESPSTSSGSSDADQRPD

261 325

RATL1d6 (235) KNORODYLNGAVSGSVQATDRLMKELRDIYRSQSFKGGNYAVELVN-DSLYDWNVKLLKVDQDSA

T21349_F25H2.8_Cel (198) KINRQOHLDGKVOGSITATDRLMKELRDIHRSEHFKNGIYTFELEKEENLYQWIKLHKVDEDS

AAF45767_EG:25E8_Dr (206) QSQRQDYLLKGSVSGSVQATDRLMKELRDIYRSDAFKKNMYSIELVN-ESIYEWNIIRLKSVDPDSP

P52483_UB6B_MOUSE (28) AAPKPEEQEERKPSATQOKNKLSSKTTAKLSTSAKRIQKELAEITLDPNPNCSAGPKGDNIE

P27924_UBC1_HUMAN (1) -----MANIAVQRIKREFKEVLKSEETSKNQIKVDLVD-----ENFT-E

CAA72184_UBCD4_Dr (1) -----MANMAVSRIKREFKEVMRSEIVQCSIKIELVN-----DSWTE

P14682_UBC3_YEAST (1) -----MSSRKSTASSLLRLQYRELTDPKKAIPSFHIELEDD-----SNIFTW

326 390

RATL1d6 (299) LHNDLQILKEKEGA-DFILNFSFKDNFPDPPFVRVVSPLVSGGYVLGGAIICMELLTKQG---

T21349_F25H2.8_Cel (263) LFEDMKKLKKDHNQ-DHLLFSFTENEKFPDPPFVRVVAAPHINQGFVLGGAIICMELLTKQG---

AAF45767_EG:25E8_Dr (270) LHSDLQMLKEKEGK-DSILNLTLEKETYPFEPFVRVWHPIISGGYVLIGGAICMELLTKQG---

P52483_UB6B_MOUSE (93) WRSTILGPPGSVYEGGVFEDDITFSSDYPEKPPKVTFRTRIYHCNINSQ-GVICLDILKDN----

P27924_UBC1_HUMAN (39) LRGETIAGPPDTPYEGGKFLBETIKVPETYPENPPKVRFITKIWHPNISSVTGAICLDILKDN----

CAA72184_UBCD4_Dr (39) LRGETIAGPPDTPYEGGKFLBETIKVPETYPENPPKVRFITKIWHPNISSVTGAICLDILKDN----

P14682_UBC3_YEAST (43) NIGVMVLNEDSIYHGGFFKAQMRFPEDFPSPQFRFTPAIYHPNVYRD-GRLCISILHQSGDPM

391 455

RATL1d6 (360) -----WSSAYSIESVIMQISATLVKKGKARVQFGANK-----SOYSLTRAQQSFKSLVQI

T21349_F25H2.8_Cel (324) -----WSSAYSIESCILQIAATLVKGRARISFDAKHT-----STYSMARAAQSFKSLQOI

AAF45767_EG:25E8_Dr (331) -----WSSAYTVEAVIMQIAATLVKKGKARIQFGATKALTQ-----GOYSLARAQSFKSLVQI

P52483_UB6B_MOUSE (153) -----WSPALTISKVLLSICSLLTDCNPADFLVGSIA-----OYLTNRAEHDRAROWT

P27924_UBC1_HUMAN (100) -----WAAAMTLRTVLLSLQALLAAAEPPDQDAVVAN-----QYKQNPPEMPQOTARLWA

CAA72184_UBCD4_Dr (100) -----WAAAMTLRTVLLSLQALLAAAEPPDQDAVVAY-----QFKDKYDLFLLTAKHWT

P14682_UBC3_YEAST (107) TDEPDAETWSPVQIVESVLTISVSLLEDPNINSEANVDAADVYRKNPEOYKQVRKMEVERSKODI

456 520

RATL1d6 (409) HEKNGWYTPPKEDG-----

T21349_F25H2.8_Cel (374) HAKSGCTFLCSTPSSHFFALHLVFFLHSDDDFFNGFLKSETFTFFKLSFRGYISSLVLYSFSRHL

AAF45767_EG:25E8_Dr (384) HEKNGWYTPPKEDG-----

P52483_UB6B_MOUSE (203) KRYAT-----

P27924_UBC1_HUMAN (150) HVIYAGAFVSSPEYTKKIENLCAMGFDRNAVIVALSSKSWDVEATATELLSN-----

CAA72184_UBCD4_Dr (150) NAYAGGPHTFPDCDSKIQRIRDMGIDEHEARAVLSKENWNLEKATEGIFS-----

P14682_UBC3_YEAST (172) PKGFIMPTSESAYISQSKLDEPESNKDMADNFWDSDLDLDDDENGSVILQDDDYDDGNNHIPFEDD

521 579

T21349_F25H2.8_Cel (439) HHPFFTRFLIPQLQPPPIPFQLIPPFLNRTKHV-----

P14682_UBC3_YEAST (237) DVYNYNDNDDDDDERIEFEDDDDDDDSIDNDSVMDRKQPKHAEDESEDVEDVERVSKKI

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FIG. 5A

RATL1d6 BLAST results/alignment w/ Drosophila protein

>GCGPROT:O46068 EG:25E8.2 PROTEIN.

Length = 394

Score = 369 bits (936), Expect = e-101

Identities = 194/403 (48%), Positives = 265/403 (65%), Gaps = 51/403 (12%)

Query: 41 LRRELKLLSIFHRGHERFRIASACLDLSCEFLLAGAGGAGAGAAPGPHLPPRGSVPGD 100
L++E+K LE IF + HERF+I ++ +DEL C F+ .G

Sbjct: 7 LKQEIKTLEKIFPKNHERFQILNSSVDELLCRFI-----DKNKG 45

Query: 101 PVRIHCNITESYPVPPPIWSVESDDPNLAALVLERLVDIKKGNTLLQLHLKRIISDLCKLY 160
IH NITE+YP+ PP+W ES++ ++ ++ L + + ++ + ++ +LC+L+

Sbjct: 46 RYDIHANITETYPSSPPVWFAESEETSVTNAVQILSNTNGRDNHVINQVGILLRELRLH 105

Query: 161 NLPQHDPDVEMLDQPLPAEQCTQEDVSSSEDE-----DEEMPEDTEDLDHYEM 206
N+P PD++ L PL + + E +EE D E+++

Sbjct: 106 NVPLPPDIDNLALPLQTTPPSASPLRCEQRPGGGGAGGGGGPHGNEETDSDQEEIEDPIG 165

Query: 207 KEEEPAGEGKK-----SEDDGIGKENLAILEKIKKNQRQDYLNQAVSGSVQATD 254
+ E+ +EG + S+ D + E+LA LEK++++QRQDYL G+VSGSVQATD

Sbjct: 166 ESEQESEGDEDLPLEMDDVRSTSKKDDMEVEHLATLEKLRSQRQDYLGKSVSGSVQATD 225

Query: 255 RLMKELRDIYRSQSFKGGNYAVELVNDSDLYDWNVLLKVDQDSALHNDLQILKEKEGADF 314
RLMKELRDIYRS +FK Y++ELVN+S+Y+WN++L VD DS LH+DLQ+LKEKEG D

Sbjct: 226 RLMKELRDIYRSDAFKKNMYSIELVNESIYEWNIRLKSVDPSPLHSDLQMLKEKEGKDS 285

Query: 315 ILLNFSFKDNFPDPPFVRVSPVLSSGGYVLGGGAICMELLTKQGWSSAYSIESVIMQIS 374
ILLN FK+ +PF+PPFVRV P++SGGYVL GGAICMELLTKQGWSSAY++E+VIMQI+

Sbjct: 286 ILLNLFKETYPPFPPFVRVHPIISGGYVLIGGAICMELLTKQGWSSAYTVEAVIMQIA 345

Query: 375 ATLVKGKARVQFGANKS----QYSLTRAQQSYKSLVQIHEKNG 413
ATLVKGKAR+QFGA K+ QYSL RAQQS+KSLVQIHEKNG

Sbjct: 346 ATLVKGKARIQFGATKALTQGGQYSLARAQQSFKSLVQIHEKNG 388

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FIG. 5B

RATL1d6 BLAST results/alignment w/ C. elegans protein

>GCGPROT:Q93571 F25H2.8 PROTEIN.

Length = 471

Score = 317 bits (805), Expect = 6e-86

Identities = 178/397 (44%), Positives = 247/397 (61%), Gaps = 49/397 (12%)

Query: 41 LRRELKLLLESIFHRGHERFRIASACLDCEFLLAGAGGAGAGAAPGPHLPGRGSPVPGD 100
L+ ++++LE +F + H RF+I SA +DELS +F+ A G

Sbjct: 7 LKEDIQVLEKLFPPKNHNRQILSASVDELSMKFINAENKG----- 46

Query: 101 PVRIHCNITESYPVPPPIWSVESDD-PNLA AVLRLVDIKKGNLTLLQHLKRIISDLCKL 159
+ + NI E+YP PPIW ESDD P + L+RL + ++ +T +L + R++SDLC

Sbjct: 47 -IIVTANIQENYPRQPPIWFSESDDDVPVIGMSLQRLTETEE-STNILHQVHRLVSDLCSEF 104

Query: 160 YNL-----PQHPDVE-----MLDQPLPAEQCTQEDVSSSEDEDEEMPEDTE 199
YNL P D++ +P+ + +V +DE+EE ED +

Sbjct: 105 YNLQMPCELPQIAPPVRDDIDEGRGSDISDTTSEPIDDDMAGDGEVDDDDDEEEEDDEDAD 164

Query: 200 -DL DHYEMKEEEPAEGKKSEDDGIGKENLAILEKIKKNQRQDYLN GAVSGSVQATDRLMK 258
D++ EM EE+P D G+ KE L +L+K+ K RQ +L+G V GS+ ATDRLMK

Sbjct: 165 GDIEIVEMAEDPTS---QHDVGVSKEGLDMLDKVSKINRQQLDQKVGQSITATDRLMK 221

Query: 259 ELRDIYRSQSFKGGNYAVELVND-SLYDWNVKKLVKVDQDSALHNDLQILKEKEGADFILL 317
E+RDI+RS+ FK G Y EL + +LY W +KL KVD+DS L D++ LK+ D +L

Sbjct: 222 EIRDIHRSEHFKNGIYTFELEKEENLYQWWIKLHKVDEDSPLFEDMKKLKDHNDHLLF 281

Query: 318 NFSFKDNFPFDPFVRVVPVLGGGYVLGGGAICMELLTKQGWSSAYSIESVIMQISATL 377
+F+F + FP DPPFVRVV+P ++ G+VLGGGAICMELLTKQGWSSAYSIES I+QI+ATL

Sbjct: 282 SFTFNEKFPCDPPFVRVVPAPHINQGFVLGGGAICMELLTKQGWSSAYSIESCILQIAATL 341

Query: 378 VKGKARVQFGA-NKSQYSLTRAQQSYKSLVQIHEKNG 413
VKG+AR+ F A + S YS+ RAQQS+KSL QIH K+G

Sbjct: 342 VKGRARISFDAKHTSTYSMARAAQSFKSLQQIHAKSG 378

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106201 645007

FIG. 6

